II. CLAIM AMENDMENTS

1-25. (Cancel).

26. (New) A fermentation process for the preparation of a desired L-amino acid selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan, and L-arginine comprising the steps of:

a) fermentation of a coryneform bacterium strain in a fermentation broth for producing the desired L-amino acid wherein the endogenous sucC and/or sucD nucleotide seqeunce are partially or completely attenuated;

b) concentration of the fermentation broth to eliminate water and increase the concentration of L-amino acids in the broth and corynbacteria, and

c) isolation of the L-amino acid, constituents of the fermentation broth and the biomass.

27. (New) The process according to claim 26, wherein other genes of the biosynthetic pathway of the desired L-amino acid of coryneform bacteria are additionally amplified.

28. (New) The process according to claim 26, wherein cornebacterium are used in which the metabolic pathways that reduce the formation of the desired L-amino acid are at least partially switched off.

29. (New) The process according to claim 26, wherein the isolated polynucleotide comprising the nucleotide sequence as set forth in SEQ ID NO: 1 is deleted.

30. (New) The process according to claim 26, wherein the isolated polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NO: 4 is deleted.

31. (New) The process according to claim 26, wherein the polynucleotide comprising a nucleotide sequence encoding the amino acid sequence as set forth in SEQ ID NO: 2 is deleted.

32. (New) The process according to claim 26, wherein the polynucleotide comprising a nucleotide sequence encoding the amino acid sequence as set forth in SEQ ID NO: 2, wherein said SEQ ID NO: 2 sequence has one or more of the following amino acid changes:

(a) the proline at position 22 is replaced by another amino acid;

(b) the glycine at position 44 is replaced by another amino acid;

(c) the alanine at position 170 is replace by another amino acids;

is deleted.

33. (New) The process according to claim 26, wherein the polynucleotide comprising the nucleotide sequence 142-1347 of SEQ ID NO: 1 is deleted.

34. (New) The process according to claim 26, wherein the expression of the sucC or sucD gene is attenuated.

35. (New) The process according to claim 26, wherein the succinyl-CoA synthetase enzymatic activity encoding the sucC or sucD gene is reduced.

36. (New) The process according to claim 26, wherein in a coryneform bacterium strain, one or more of the genes selected from the group is overexpressed:

(a) the dapA gene encoding dihydrodipicolinate synthase,

(b) the gap gene encoding glyceraldehyde 3-phosphate dehydrogenase,

(c) the tpi gene encoding triose phoshate isomerase,

(d) the pgk gene encoding 3-phosphoglycerate kinase,

(e) the zwf gene encoding glucose 6-phosphate dehydrogenase,

(f) the mqo gene encoding malate:quinone oxidoreductase,

(g) the lysE-gene coding for L-lysine export,

(h) the gene lysC coding for a feedback resistant aspartate kinase, and

(i) the gene zwa1 coding for the Zwa1-protein.

37. (New) The process according to claim 26, wherein in a coryneform bacterium strain, one or more of the genes selected from the group is attenuated:

(a) the gene pck coding for phosphoenol pyruvate carboxykinase,

(b) the gene pgi coding for glucose-6-phosphate isomerase,

(c) the gene poxB coding for pyruvate-oxidase, and

(d) the gene zwa2 coding for the Zwa2-protein.

38. (New) The process according to claim 26, wherein said coryneform bacteria are of the species Corynebacterium glutamicum.

39. (New) A method for the preparation of L-amino acids selected from the group consisting of L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan, and L-arginine comprising culturing a coryneform bacterium strain in a medium suitable to produce said L-amino acids and wherein the endogenous sucC and/or sucD nucleotide seqeunce are partially or completely attenuated.

40. (New) The method of claim 39, further comprising isolating the L-amino acids.

41. (New) The method of claim 39, wherein the coryneform bacterium have been transformed with a plasmid vector selected from the group consisting of:

(a) the integration vector pCRBluntsucCint as show in Figure 1 and which has been deposited in E. coli as DSM 13750; and

(b) the vector pK18mobsacBsucDdel as shown in Figure 2 and which has been deposited in E. coli as DSM 13749 in order to delete the endogenous sucC and/or sucD nucleotide seqeunce.

42. (New) The method of claim 39, wherein the coryneform bacterium strain is Corynebacterium glutamicum.

43. (New) A process for producing L-amino acids comprising:

(a) transforming a coryneform bacterium with a plasmid vector selected from the group consisting of:

(i) the integration vector pCRBluntsucCint as show in Figure 1 and which has been deposited in E. coli as DSM 13750; and

(ii) the vector pK18mobsacBsucDdel as shown in Figure 2 and which has been deposited in E. coli as DSM 13749 in order to delete the endogenous sucC and/or sucD nucleotide seqeunce;

(b) culturing said bacterium in a medium suitable for producing said L-amino acids;

(c) isolating the L-amino acids.

44. (New) The process according to claim 43, wherein the isolated L-amino acid is L-lysine.

45. (New) The process according to claim 43, wherein the coryneform bacterium is Corynebacterium glutamicum.